Matrix-assisted laser desorption ionization-time of flight mass spectrometry for fast and accurate identification of Pseudallescheria/Scedosporium species

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Résumé en anglais	Current identification of Scedosporium spp. based on morphological characteristics fails todetect emerging species described using multi-locus sequencing (MLS). Among the 8 recently described phylogenetic species which grouped in five different clades, only Scedosporium apiospermum (clade 4) and Pseudallescheria boydii (clade 5) are known as common pathogens in humans, while the 6 others are emerging, including for exemple Scedosporium aurantiacum (clade 1), Pseudallescheria minutispora (clade 2), or Scedosporium dehoogii (clade 3). In addition, another Scedosporium species, Scedosporium prolificans, which is also common human pathogen but is not included in these clades, cannot be differentiated from those belonging to the above-mentioned clades using morphological techniques. However, accurate identification is important because antifungal drug susceptibility patterns may vary with the species. Matrix-assisted laser desorption ionization-time mass spectrometry (MALDI-TOF MS), allows rapid and reliable identification of microorganisms. We postulated that this method, can also discriminate species of Scedosporium just as we showed for Aspergillus species A set of 7 reference strains belonging to 5 clinically relevant species (S. apiospermum, P. boydii, S. aurantiacum, S. prolificans, P. minutispora) was used to build a reference database Profiles from each referenced strain at different age of the cultures (Days 3, 5, 7) were analyzed to identify species specific discriminating peaks. The spectra of 50 strains (25 P. boydii, 19 S. apiospermum, 3 S. aurantiacum, 2 P.minutispora, 1 S. prolificans) previously identified with MLS (tubulin and/or ITS) were compared to that of each of the reference strains. This database allowed correct identification of 48/50 strains (96%), with no misidentification. Our results, obtained using a simple protocol with no extraction step showed that MALDI-TOF-MS is a powerful tool for rapid identification of clinically relevant species of Scedosporium, including those emerging that cannot currently be identified by micoscopic examination.

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